

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant must provide:**

- ☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123  
For CRF submission help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/347,780DATE: 03/16/95  
TIME: 19:19:13

INPUT SET: S2790.raw

# 4

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Bartley, Timothy D.  
Bogenberger, Jakob M.  
Bosselman, Robert A.  
Hunt, Pamela  
Kinstler, Olaf B.  
Samal, Babru B.

(ii) TITLE OF INVENTION: Compositions and Methods for Stimulating  
Megakaryocyte Growth and Differentiation

(iii) NUMBER OF SEQUENCES: 34

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.  
(B) STREET: 1840 Dehavilland Drive  
(C) CITY: Thousand Oaks  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91320-1789

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cook, Robert R.  
(C) REFERENCE/DOCKET NUMBER: A-290-C

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/347,780DATE: 03/16/95  
TIME: 19:19:16

INPUT SET: S2790.raw

47 (D) TOPOLOGY: linear  
48  
49 (ii) MOLECULE TYPE: protein  
50  
51  
52  
53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
54  
55 Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp  
56 1 5 10 15  
57  
58 Ser His Val Leu His Xaa Arg Leu Xaa Gln Xaa Pro Asp Ile Tyr  
59 20 25 30  
60  
61 (2) INFORMATION FOR SEQ ID NO:2:  
62  
63 (i) SEQUENCE CHARACTERISTICS:  
64 (A) LENGTH: 21 amino acids  
65 (B) TYPE: amino acid  
66 (C) STRANDEDNESS: single  
67 (D) TOPOLOGY: linear  
68  
69 (ii) MOLECULE TYPE: protein  
70  
71  
72  
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
74  
75 Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp  
76 1 5 10 15  
77  
78 Ser His Val Leu His  
79 20  
80  
81 (2) INFORMATION FOR SEQ ID NO:3:  
82  
83 (i) SEQUENCE CHARACTERISTICS:  
84 (A) LENGTH: 17 amino acids  
85 (B) TYPE: amino acid  
86 (C) STRANDEDNESS: single  
87 (D) TOPOLOGY: linear  
88  
89 (ii) MOLECULE TYPE: protein  
90  
91  
92  
93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
94  
95 Thr Gln Lys Glu Gln Thr Lys Ala Gln Asp Val Leu Gly Ala Val Ala  
96 1 5 10 15  
97  
98 Leu  
99

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PATENT APPLICATION US/08/347,780DATE: 03/16/95  
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100  
101 (2) INFORMATION FOR SEQ ID NO:4:  
102  
103 (i) SEQUENCE CHARACTERISTICS:  
104 (A) LENGTH: 17 base pairs  
105 (B) TYPE: nucleic acid  
106 (C) STRANDEDNESS: single  
107 (D) TOPOLOGY: linear  
108  
109 (ii) MOLECULE TYPE: cDNA  
110  
111  
112  
113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
114  
115 GCNCCNCCNG CNTGYGA 17  
116  
117 (2) INFORMATION FOR SEQ ID NO:5:  
118  
119 (i) SEQUENCE CHARACTERISTICS:  
120 (A) LENGTH: 21 base pairs  
121 (B) TYPE: nucleic acid  
122 (C) STRANDEDNESS: single  
123 (D) TOPOLOGY: linear  
124  
125 (ii) MOLECULE TYPE: cDNA  
126  
127  
128  
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
130  
131 GCARTGYAAC ACRTGNGART C 21  
132  
133 (2) INFORMATION FOR SEQ ID NO:6:  
134  
135 (i) SEQUENCE CHARACTERISTICS:  
136 (A) LENGTH: 21 amino acids  
137 (B) TYPE: amino acid  
138 (C) STRANDEDNESS: single  
139 (D) TOPOLOGY: linear  
140  
141 (ii) MOLECULE TYPE: protein  
142  
143  
144  
145 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
146  
147 Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp  
148 1 5 10 15  
149  
150 Ser His Val Leu His  
151 20  
152

RAW SEQUENCE LISTING  
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153 (2) INFORMATION FOR SEQ ID NO:7:

154

155 (i) SEQUENCE CHARACTERISTICS:

156 (A) LENGTH: 21 base pairs

157 (B) TYPE: nucleic acid

158 (C) STRANDEDNESS: single

159 (D) TOPOLOGY: linear

160

161 (ii) MOLECULE TYPE: cDNA

162

163

164

165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

166

167 GTACGCGTTC TAGANNNNNN T

21

168

169 (2) INFORMATION FOR SEQ ID NO:8:

170

171 (i) SEQUENCE CHARACTERISTICS:

172 (A) LENGTH: 21 base pairs

173 (B) TYPE: nucleic acid

174 (C) STRANDEDNESS: single

175 (D) TOPOLOGY: linear

176

177 (ii) MOLECULE TYPE: cDNA

178

179

180

181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

182

183 AGTTTACTGA GGACTCGGAG G

21

184

185 (2) INFORMATION FOR SEQ ID NO:9:

186

187 (i) SEQUENCE CHARACTERISTICS:

188 (A) LENGTH: 30 base pairs

189 (B) TYPE: nucleic acid

190 (C) STRANDEDNESS: single

191 (D) TOPOLOGY: linear

192

193 (ii) MOLECULE TYPE: cDNA

194

195

196

197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

198

199 TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

200

201 (2) INFORMATION FOR SEQ ID NO:10:

202

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 29 base pairs

205 (B) TYPE: nucleic acid

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206 (C) STRANDEDNESS: single  
207 (D) TOPOLOGY: linear  
208  
209 (ii) MOLECULE TYPE: cDNA  
210  
211  
212  
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
214  
215 TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT 29  
216  
217 (2) INFORMATION FOR SEQ ID NO:11:  
218  
219 (i) SEQUENCE CHARACTERISTICS:  
220 (A) LENGTH: 20 base pairs  
221 (B) TYPE: nucleic acid  
222 (C) STRANDEDNESS: single  
223 (D) TOPOLOGY: linear  
224  
225 (ii) MOLECULE TYPE: cDNA  
226  
227  
228  
229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
230  
231 TGCGACCTCC GAGTCCTCAG 20  
232  
233 (2) INFORMATION FOR SEQ ID NO:12:  
234  
235 (i) SEQUENCE CHARACTERISTICS:  
236 (A) LENGTH: 23 base pairs  
237 (B) TYPE: nucleic acid  
238 (C) STRANDEDNESS: single  
239 (D) TOPOLOGY: linear  
240  
241 (ii) MOLECULE TYPE: cDNA  
242  
243  
244  
245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
246  
247 GAGTCCTCAG TAAACTGCTT CGT 23  
248  
249 (2) INFORMATION FOR SEQ ID NO:13:  
250  
251 (i) SEQUENCE CHARACTERISTICS:  
252 (A) LENGTH: 20 base pairs  
253 (B) TYPE: nucleic acid  
254 (C) STRANDEDNESS: single  
255 (D) TOPOLOGY: linear  
256  
257 (ii) MOLECULE TYPE: cDNA  
258